REMARKS

Status of the Claims

Claim 1 has been amended without prejudice to or disclaimer of the subject matter therein as described elsewhere. Responsive to the restriction requirement issued June 11, 2002, Claims 19-20 have been cancelled without prejudice to or disclaimer of the subject matter therein and new Claims 21-22 have been added. Support for the amendments and new claims can be found in the specification as described below. Claims 1-18 and 21-22 are now pending. The Examiner is respectfully requested to enter the above amendments and new claims to further prosecution. The amendments and new claims were not presented earlier because they were made in response to the Examiner's suggestion made during the February 21, 2003 Interview.

The Examiner's comments in the Final Office Action are addressed below in the order set forth therein.

Examiner Interview

Applicants wish to thank the Examiner for the interview conducted on February 21, 2003, with inventors Bill Evans and Oliver McDonald, and Applicants' representatives, Scott Elmer, Murray Spruill, and Eric Kron. During the interview, the Examiner indicated that claims reciting that the PCR primers anneal to a region of the DNA segment outside the polymorphism would be free of the art. Applicants wish to thank the Examiner for the helpful suggestion.

The Rejections of the Claims Under 35 U.S.C. § 103 Should Be Withdrawn

Claims 1-16 stand rejected under 35 U.S.C. § 103 over Patel *et al.* (1991) *Nucleic Acids Res.*, 19:3561-3567 in view of Michalatos-Beloin *et al.* (1996) *Nucleic Acids Res.* 24:4841-4843.

Although Applicants respectfully traverse the rejection, for the sake of expediting prosecution, Claim 1 has been amended to recite that "the PCR amplification is performed with a first primer capable of annealing to a region adjacent to the first NP and distal to the second NP and a second primer capable of annealing to a region adjacent to the second NP and distal to the first NP...." Support for this amendment can be found in the specification, paragraph spanning pages 3-4, as well as in original Claim 19.

Applicants have further added new Claim 21, which specifies that "the DNA segment further comprises a DNA sequence immediately 5' to the first NP that encompasses an annealing site for a primer and a DNA sequence immediately 3' to the second NP that encompasses an annealing site for a primer...." Support for this claim can be found in the specification on page 7, lines 10-12. New Claim 22 has been added which depends from Claim 21 and recites various lengths for the DNA sequence. Support for this claim can be found in the specification on page 7, lines 12-14.

The amendment to Claim 1 and the subject matter of Claim 21 are in accordance with the Examiner's suggestion for overcoming the rejection. Consequently, Applicants respectfully request that the rejection be withdrawn.

Claim 17 is rejected under 35 U.S.C. § 103 over Patel and Michalatos-Beloin in further view of Krynetski *et al.* (1995) *Proc. Natl. Acad. Sci.*, 92:949-953. Applicants respectfully traverse.

As described above, amended Claim 1 and new Claim 21 alleviate the Examiner's concerns regarding Patel and Michalatos-Beloin. Krynetski merely teaches a point mutation of the TPMT gene and, because the rejection based upon the primary references has been obviated, the rejection should be withdrawn.

Claim 18 is rejected under 35 U.S.C. § 103 over Patel and Michalatos-Beloin in further view of Martin *et al.* (2000) *Am. J. Hum. Genet.*, 67:383-394. Applicants respectfully traverse.

Amended Claim 1 and new Claim 21 alleviate the Examiner's concerns regarding Patel and Michalatos-Beloin. Martin teaches SNPs in the region surrounding the APOE gene and, because the rejection based upon the primary references has been obviated, the rejection should be withdrawn.

CONCLUSION

In view of the aforementioned amendments and remarks, Applicants respectfully submit that the rejections of the claims under 35 U.S. C. § 103 are obviated. The Examiner is respectfully requested enter the above amendments because they will place the application in condition for allowance. Applicants further request that the rejections be withdrawn and that the Examiner allow claims 1-18 and 21-22. Early notice to this effect is solicited.

If in the opinion of the Examiner a telephone conference would expedite the prosecution of the subject application, the Examiner is invited to call the undersigned.

It is not believed that extensions of time or fees for net addition of claims are required, beyond those, which may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-0605.

Respectfully submitted,

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CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: **BOX AF**, Commissioner for Patents, Washington, DC 20231, on March 11, 2003.

Nora C. Martinez

Version with Markings to Show Changes Made:

In the Specification:

Please replace the paragraph beginning on Page 1, Lines 1 through 4, with the following paragraph:

FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made in part with U.S. Government support under National Institutes of Health grants GM 61393, R37 CA36401 and R01 CA78224, and Cancer Center support grant CA21765. The Government may have certain rights in this invention.

In the Claims:

Please amend Claim 1 as follows:

1. (Once Amended) A method for determining the haplotype structure of a contiguous DNA segment comprising a first nucleotide polymorphism (NP) and a second NP separated by at least 200 nucleotides, said method comprising:

(a) obtaining a DNA sample comprising said contiguous DNA segment;

(b) using said DNA sample as a template for polymerase chain reaction (PCR) amplification of a DNA fragment comprising said contiguous DNA segment,

wherein the PCR amplification is performed with

a first primer capable of annealing to a region adjacent to the first NP and distal to the second NP and

a second primer capable of annealing to a region adjacent to the second NP and distal to the first NP;

(c) ligating the ends of said DNA fragment to each other so as to produce a circular DNA molecule; and

(d) determining the haplotype of said first NP and said second NP.